



RECEIVED  
FEB 10 2003  
TECH CENTER 1600/2900

TRFP CHAIN 1, LEADER A

10	20	30	40	50	60
CTGCATCATGAAGGGGGCTCGTGTTCCTCGTGCTTCTCTGGGCTGCCTTGCTCTTGATCTG					
C I M K G A R V L V L L W A A L L L I W					
<hr/>					
70	80	90	100	110	120
GGGTGGAAATTGTGAAATTTGCCAGCCGTGAAGAGGGATGTTGACCTATTCCTGACGGG					
G G N C E I C P A V K R D V D L F L T G					
<hr/>					
130	140	150	160	170	180
AACCCCGACGPATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGTATTGGA					
T P D E Y V E Q V A Q Y K A L P V V L E					
<hr/>					
190	200	210	220	230	240
AAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAAGGAGAA					
N A R I L K N C V D A K M T E E D K E N					
<hr/>					
250	260	270	280	290	300
TGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCATCACTG					
A L S L L D K I Y T S P L C -					
<hr/>					
310	320	330	340	350	360
CCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTGCCATGT					
<hr/>					
370	380	390	400	410	
CCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTGGCAATTCAAACAAAAAAA					

Fig. 1



TRFP CHAIN 1, LEADER B

10 20 30 40 50 60  
GGCCTGGCGGTGCTCCTGGAAAAGGATGTTAGACGCAGCCCTCCCACCCTGCCCTACTGT  
A W R C S W K R M L D A A L P P C P T V

70 80 90 100 110 120  
TGCGGCCACAGCAGATTGTGAAATTGCCCAGCCGTGAAGAGGGATGTTGACCTATTCTT  
A A T A D C E I C P A V K R D V D L F L

130 140 150 160 170 180  
GACGGGAACCCCGACGAATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGT  
T G T P D E Y V E Q V A Q Y K A L P V V

190 200 210 220 230 240  
ATTGGAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAA  
L E N A R I L K N C V D A K M T E E D K

250 260 270 280 290 300  
GGAGAATGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCA  
E N A L S L L D K I Y T S P L C - R S H

310 320 330 340 350 360  
TCACTGCCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTG

370 380 390 400 410 420  
CCATGTCCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTTGCAATTCAAACAAAA

Fig. 2



TRFP CHAIN 2, LONG FORM

10	20	30	40	50	60
TGACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGT					
D T M R G A L L V L A L L V T Q A L G V					
<hr/>					
70	80	90	100	110	120
CAAGATGGCGGAAACTTGCCCCATTTTTTATGACGTCTTTTTTGCGGTGGCCAATGGAAA					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
TGAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGC					
E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
CATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGG					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
ACTAGTCATGACAACCATCAGCTCCAGCAAAGATTGCATGGGTGAAGCAGTTCAGAACAC					
L V M T T I S S S K D C M G E A V Q N T					
310	320	330	340	350	360
CGTAGAAGATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCTTC					
V E D L K L N T L G R -					
370	380	390	400	410	420
TGAGCCCCATCCTCCTGCCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCT					
430	440	450	460	470	
CACCTAATTCACTCTCAATCAGGCTGACTAGAATAAAATAACTGCATCTTAAAAAA					

Fig. 3



TRFP I CHAIN 2, SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC					
D T M R G A L L V L A L L V T Q A L G V					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGC GGTGGCCAATGGAAAT					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC					
E L L L D L S L T K V N A T E P E R V A					
190	200	210	220	230	240
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGGA					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGATAGCCATCAACGAATATTGCATGGGTGAAGCAGTTCAGAACACCGTAGAA					
L V M I A I N E Y C M G E A V Q N T V E					
310	320	330	340	350	360
GATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCC					
D L K L N T L G R -					
370	380	390	400	410	420
CATCCTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAA					
430	440	450	460		
TTCACCTCAATCAGGCTGACTAGATAAAATAACTGCATCTTAAAAAA					

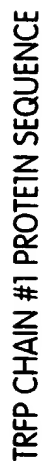
Fig. 4



TRFP CHAIN 2, TRUNCATED SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC					
D T M R G A L L V L A L L V T O A L G V					
<hr/>					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGCGGTGGCCAATGGAAT					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC					
E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGATGGA					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGCCATCAACGAATATTGCATGGGTGAAGCAGTTTCAGAACACCGTAGAAGATC					
L V M P S T N I A W V K Q F R T P -					
310	320	330	340	350	360
TCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCCCATC					
370	380	390	400	410	420
CTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAATTCA					
430	440	450	460		
CTCTCAATCAGGCTGACTAGATAAAATAAAGTGCATCTTAAAAAA					

Fig. 5

[illegible]

**Fig. 6**



TRFP CHAIN #2 PROTEIN SEQUENCES

	-10																																						
	D T M R G A L L V L A L L V T Q A L G																																						
C2 Leader	5	10	15	20	25	30	35	40																															
C2L	V	R	M	A	E	T	C	P	I	F	Y	D	V	F	F	A	V	A	N	G	N	E	L	L	D	L	S	L	T	R	V	N	A	T	E	P	E	R	T
C2S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C2ST	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
PRO.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

Fig. 7A

**Fig. 7B**





PATIENT # 131.2 2° (TRFP:1°)

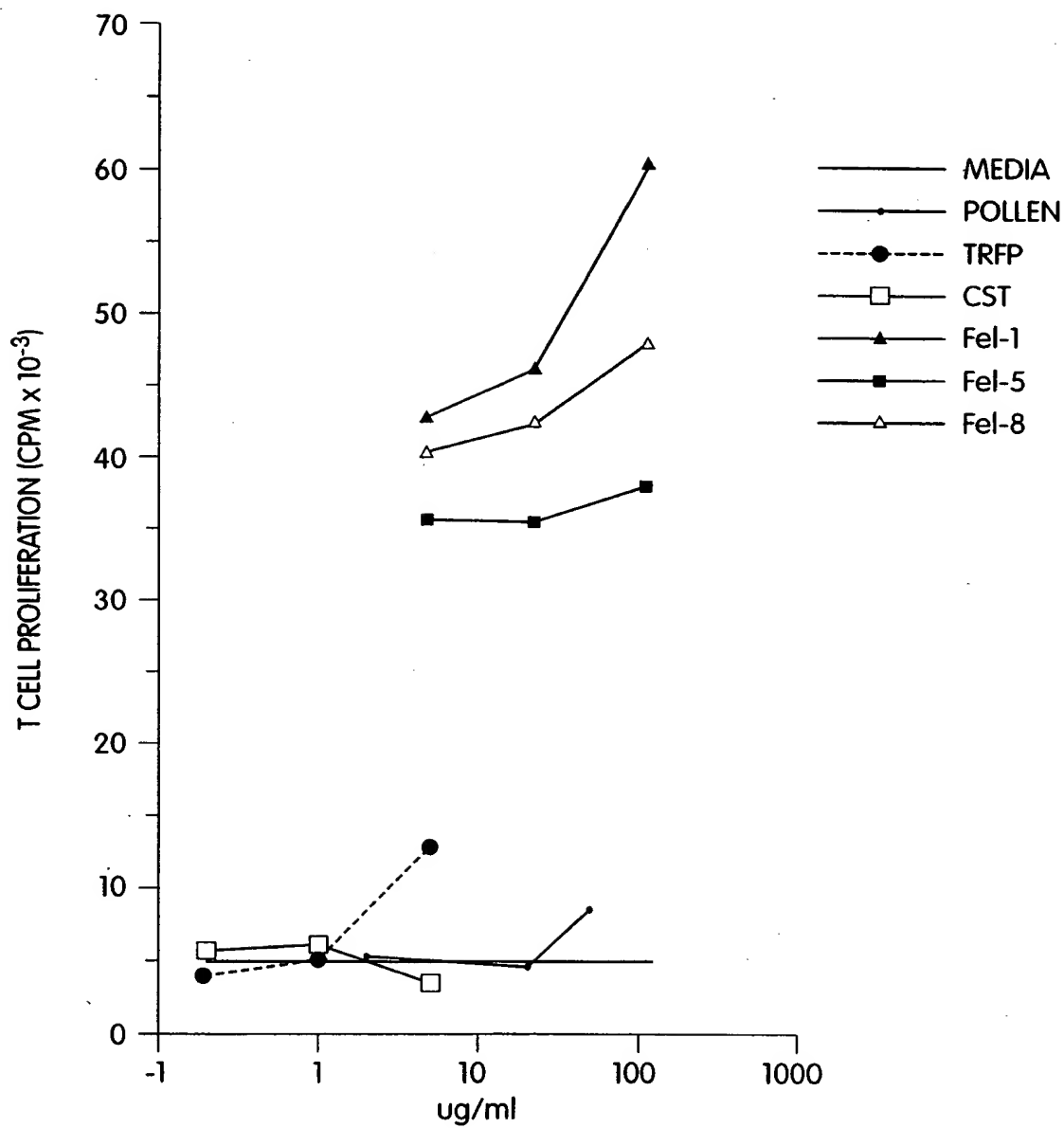


Fig. 8

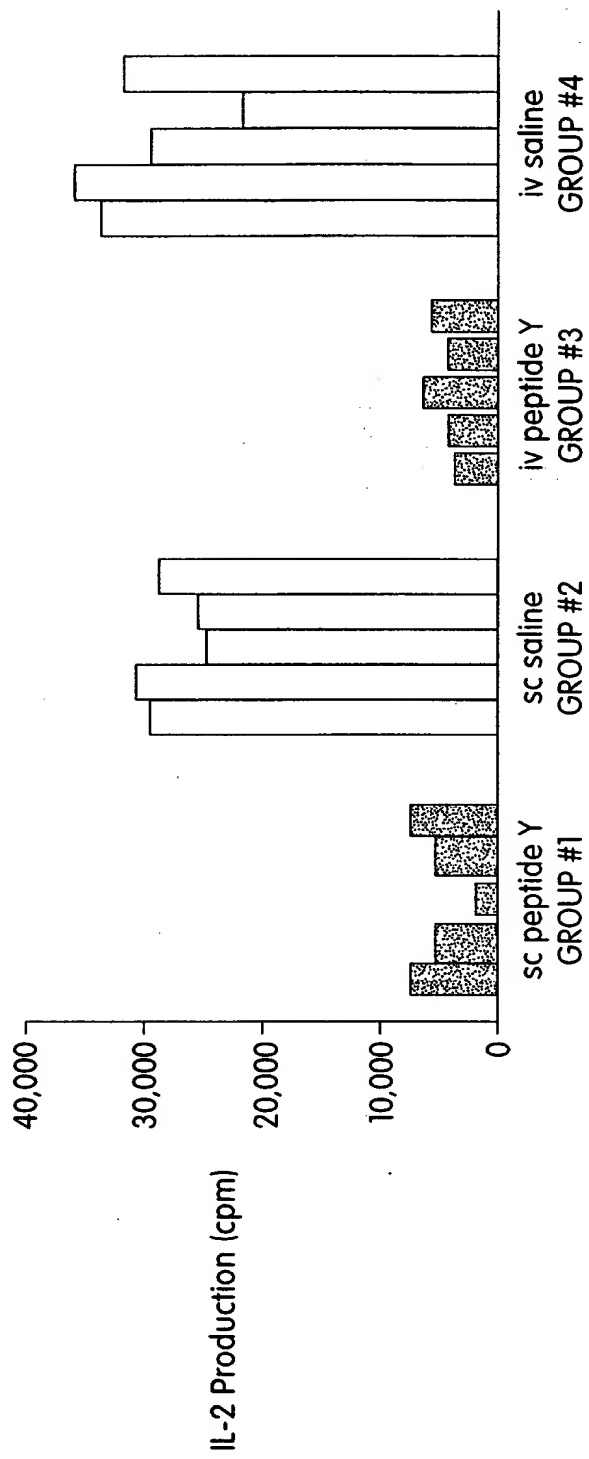


Fig. 9

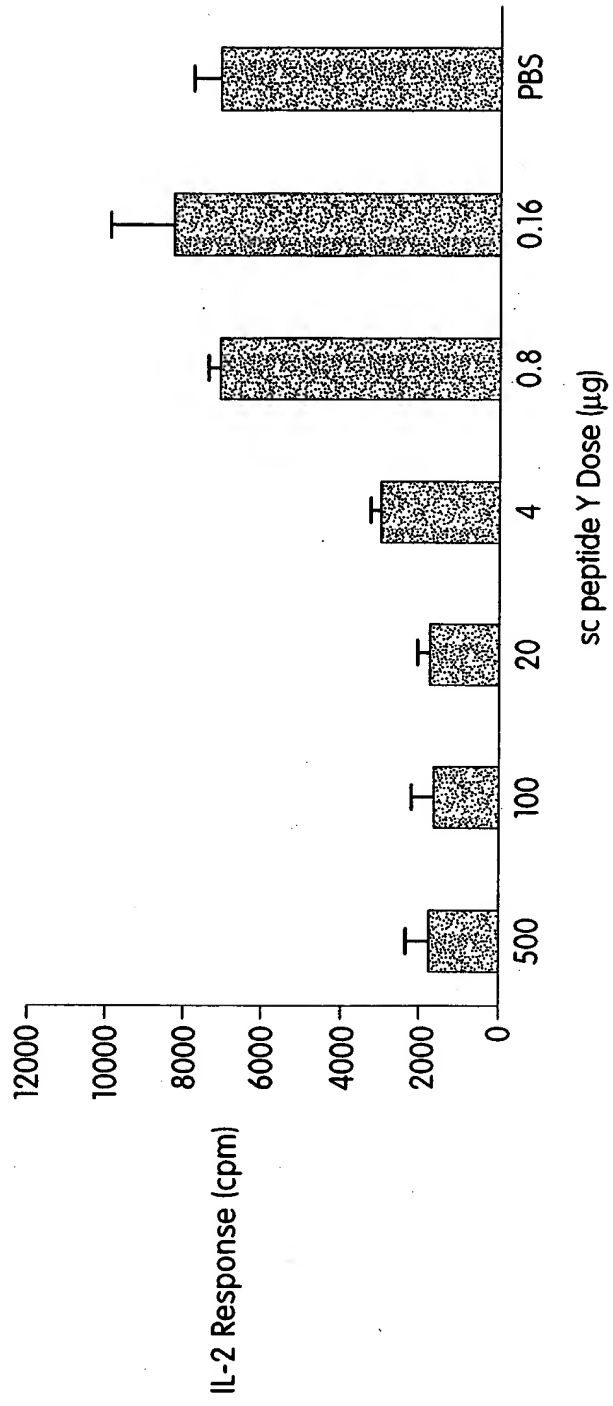


Fig.10

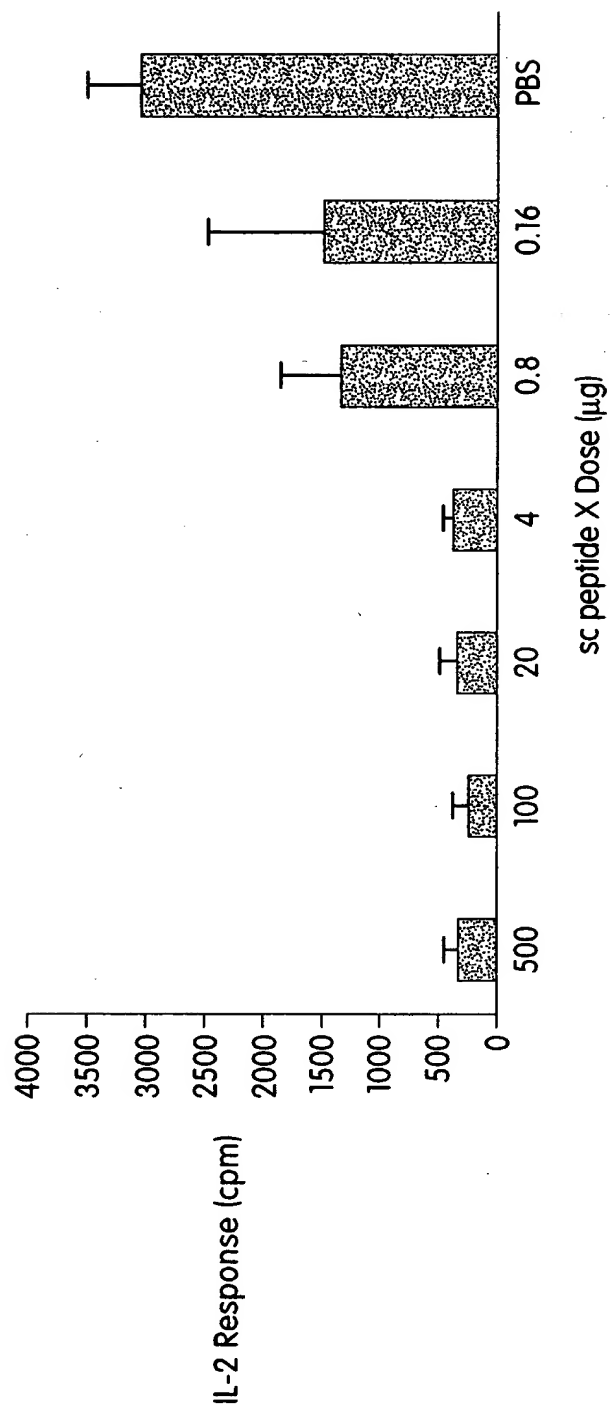


Fig.11

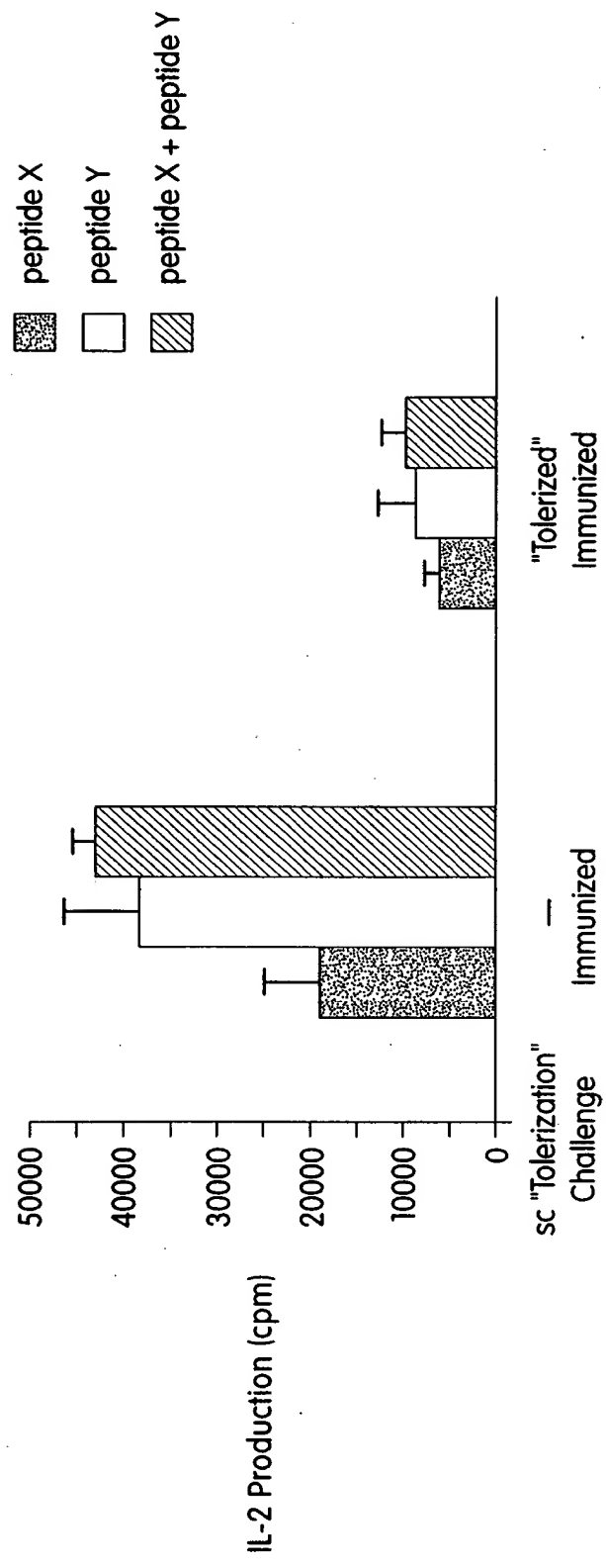


Fig.12

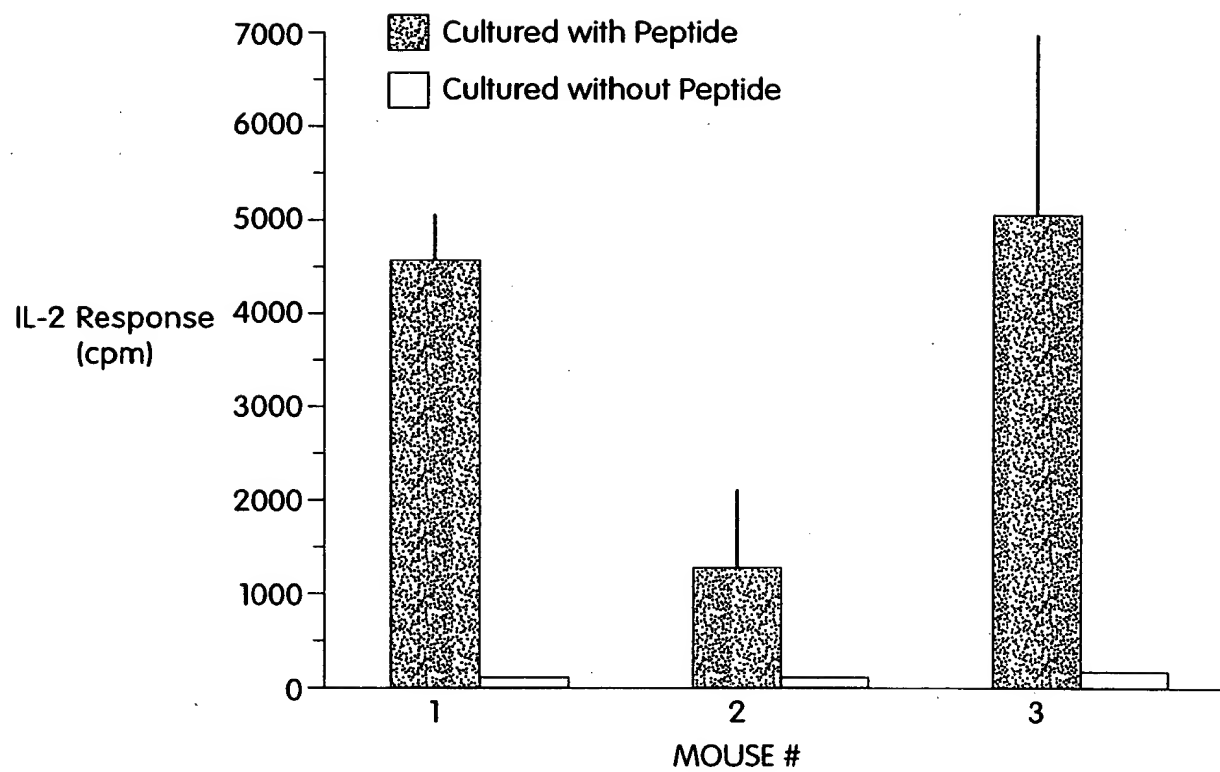


Fig. 13

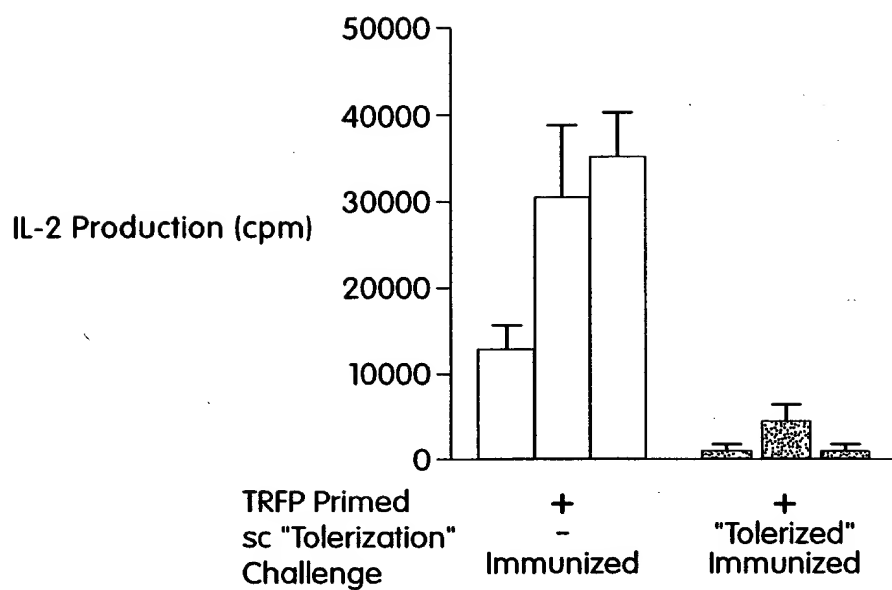


Fig. 14A

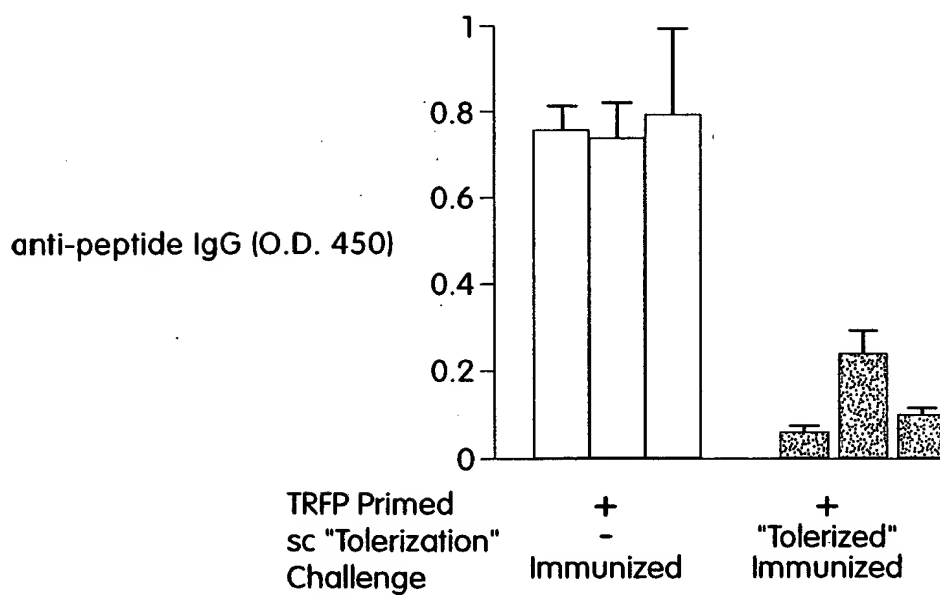


Fig. 14B

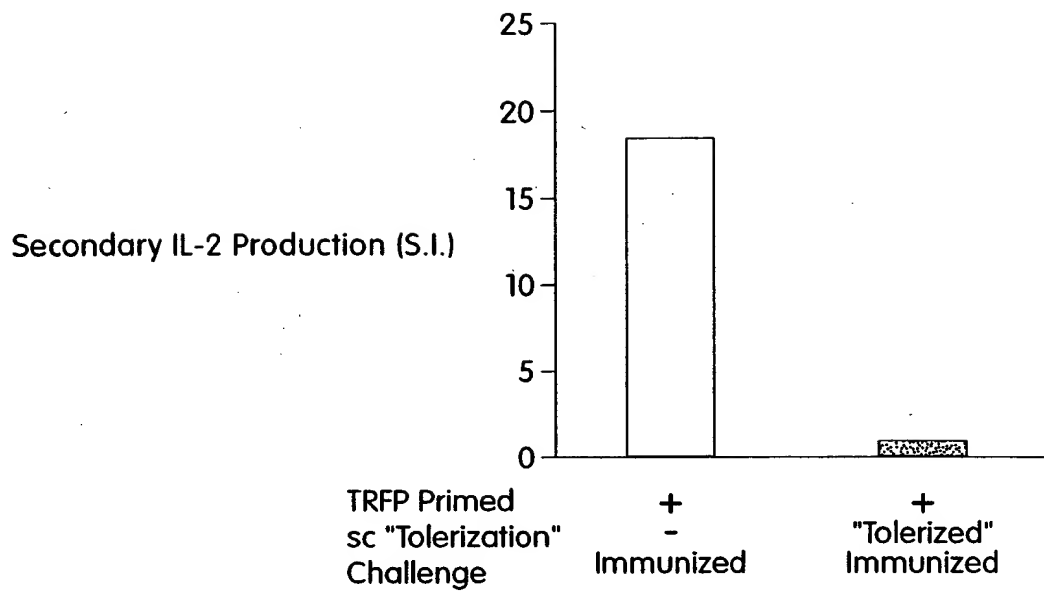


Fig. 15A

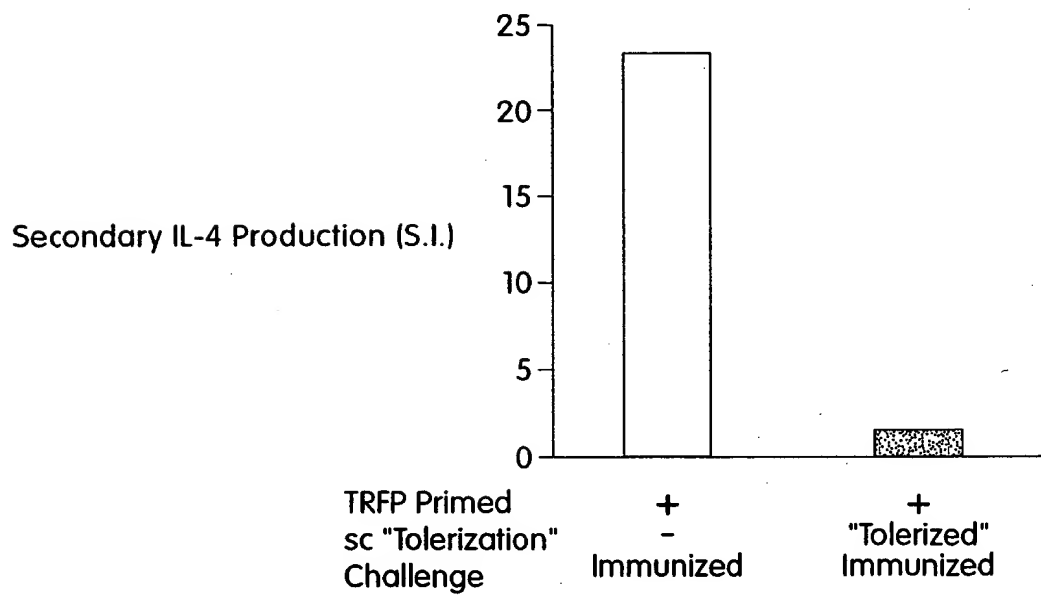


Fig. 15B



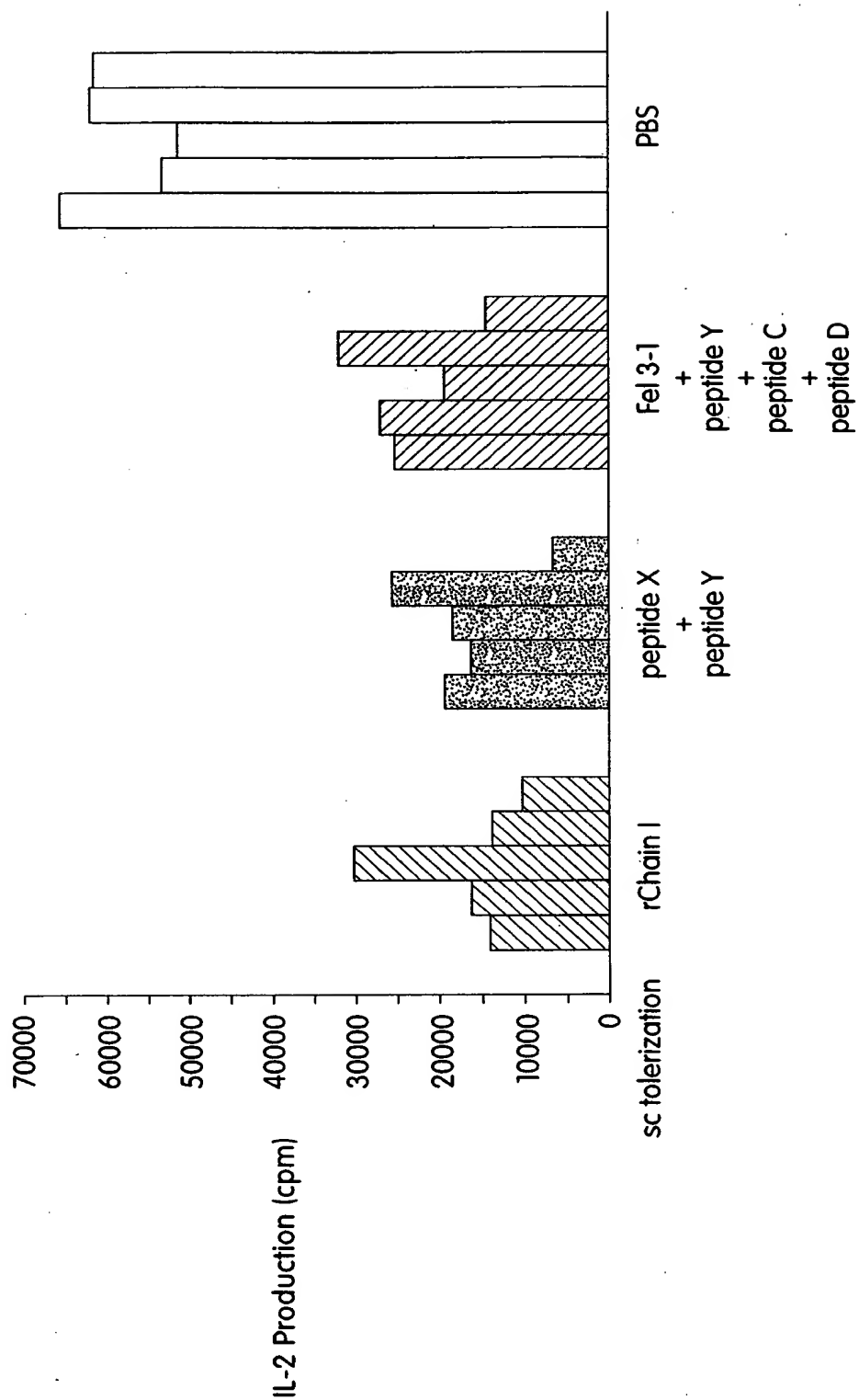


Fig. 16



SEQUENCE

PEPTIDE  
NAME

<b>X</b>	<b>KRDVDLFLTGTPDEYVEQVAQYKALPV</b>
<b>Y</b>	<b>KALPVVLENARILKNCVDAKMTEEDKE</b>
<b>Z</b>	<b>FFAVANGNELLLDLSLTKVNATEPER</b>
<b>A</b>	<b>EEDKENALSLLDKIYTSPL</b>
<b>B</b>	<b>MGEAVQNTVEDLKLNTLGR</b>
<b>C</b>	<b>EEDKENALSLLDKIYT</b>
<b>D</b>	<b>NALSLLDKIYTSPL</b>

Fig. 17



**Fel 32 VKMAETCPIFYDVFFAVA**  
**Fel 33 FYDVFFAVANGNELLLD**  
**Fel 34 NGNELLLDLSLTKVNATE**  
**Fel 35 SLTKVNATEPERTAMKKI**  
**Fel 36 ERTAMKKIQDCYVENGL**  
**Fel 37 QDCYVENGLISRVLDGLV**  
**Fel 38 ISRVLDGLVMTTISSSKDCM**  
**Fel 38-1 ISRVLDGLVMIAINE\*\*DCM**  
**Fel 39 MTTISSSKDCMGEAVQNTTEVELDKLNTLGF**  
**Fel 39.1 MIAINE\*\*DCMGEAVQNTTEVELDKLNTLGF**

**Fig. 18**

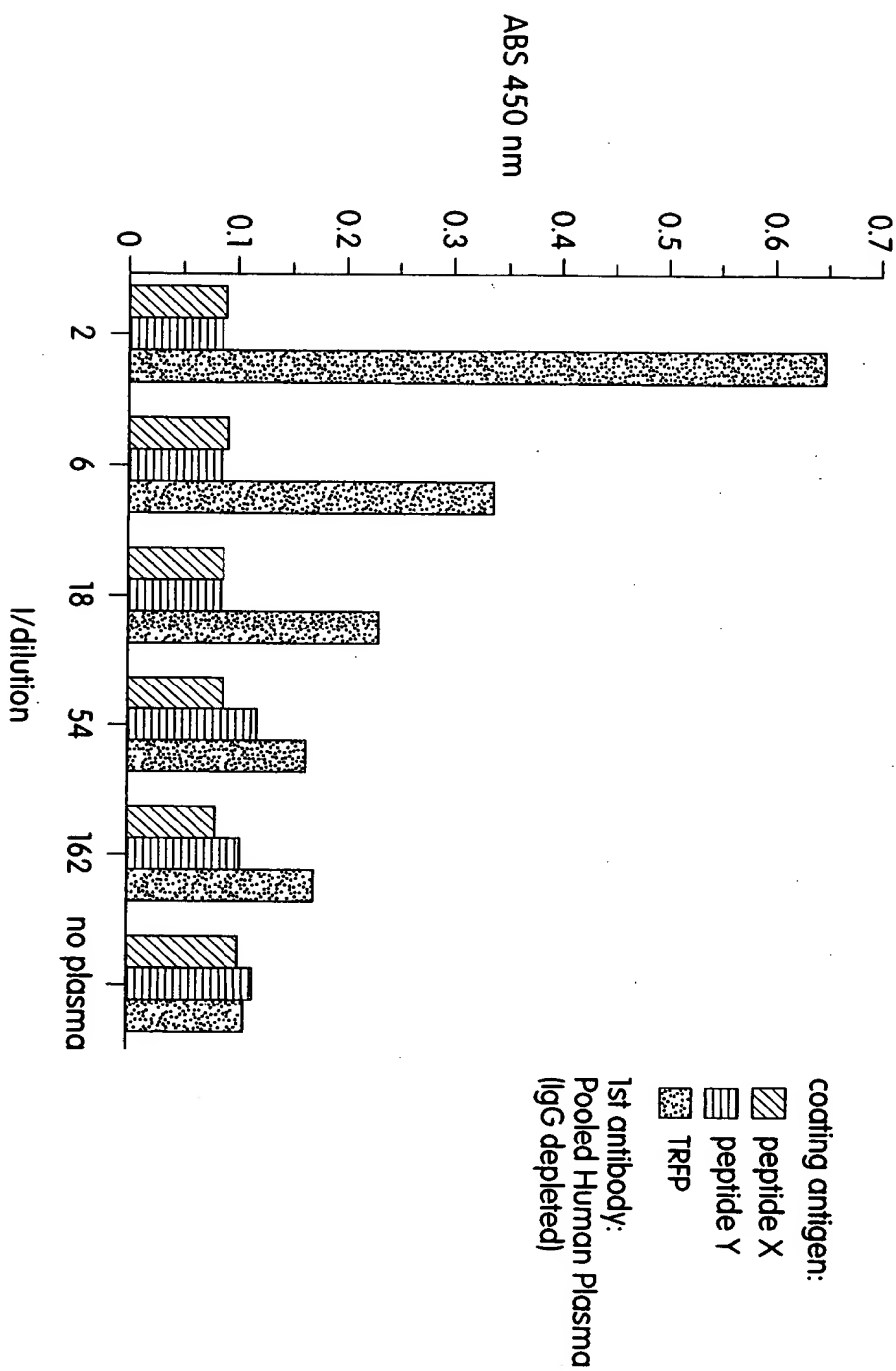


Fig. 19

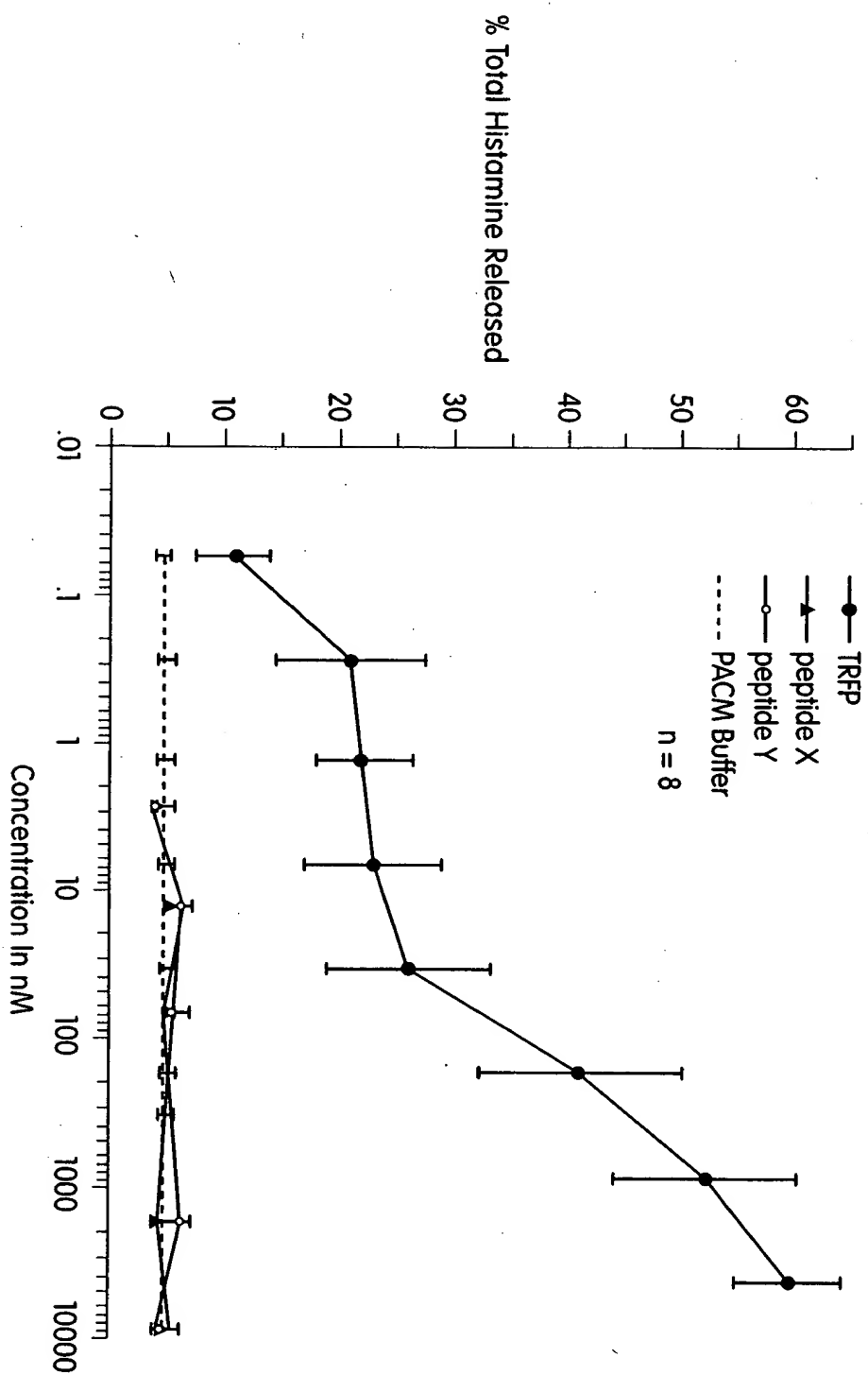


Fig. 20

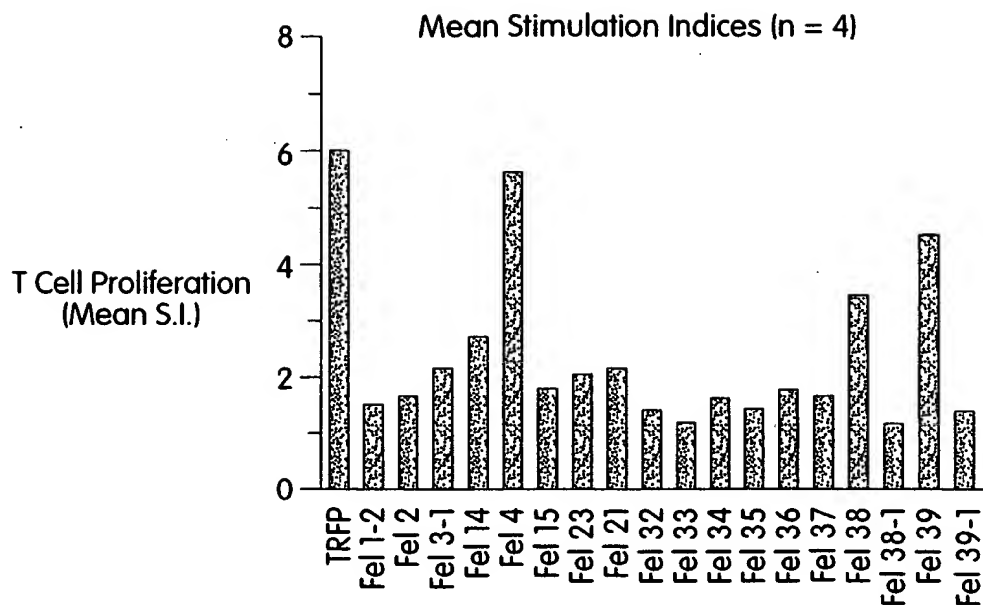


Fig. 21A

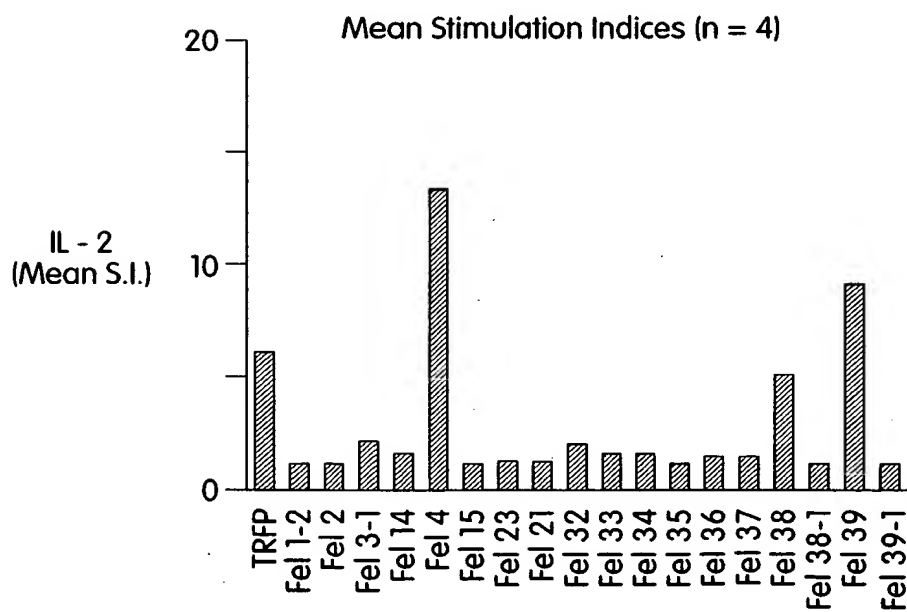


Fig. 21B

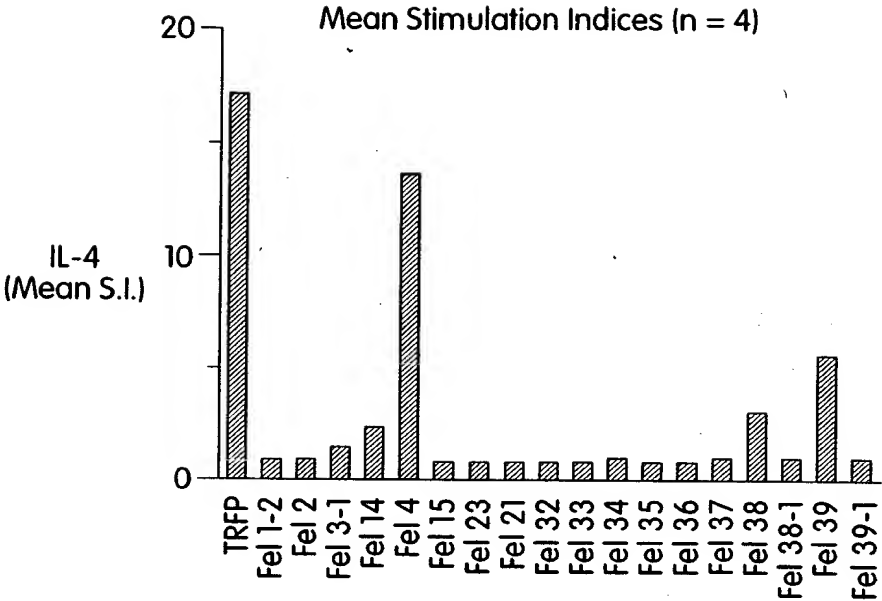


Fig. 21C

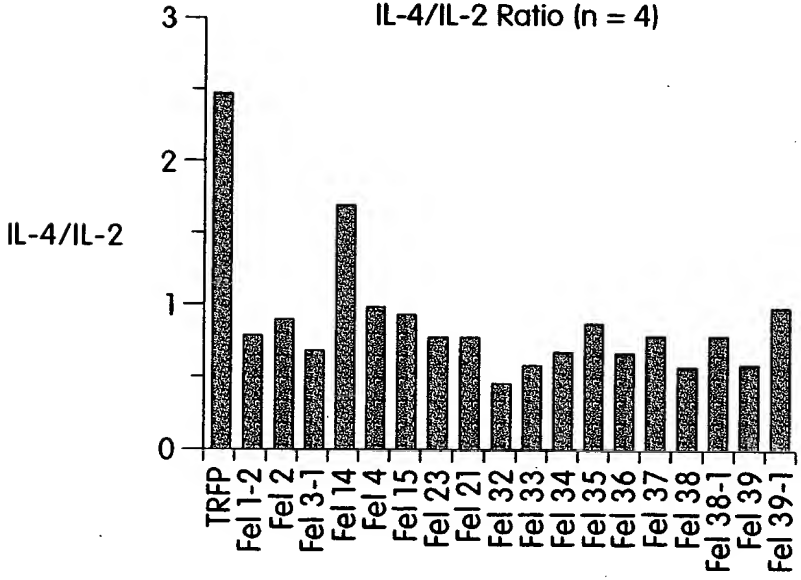
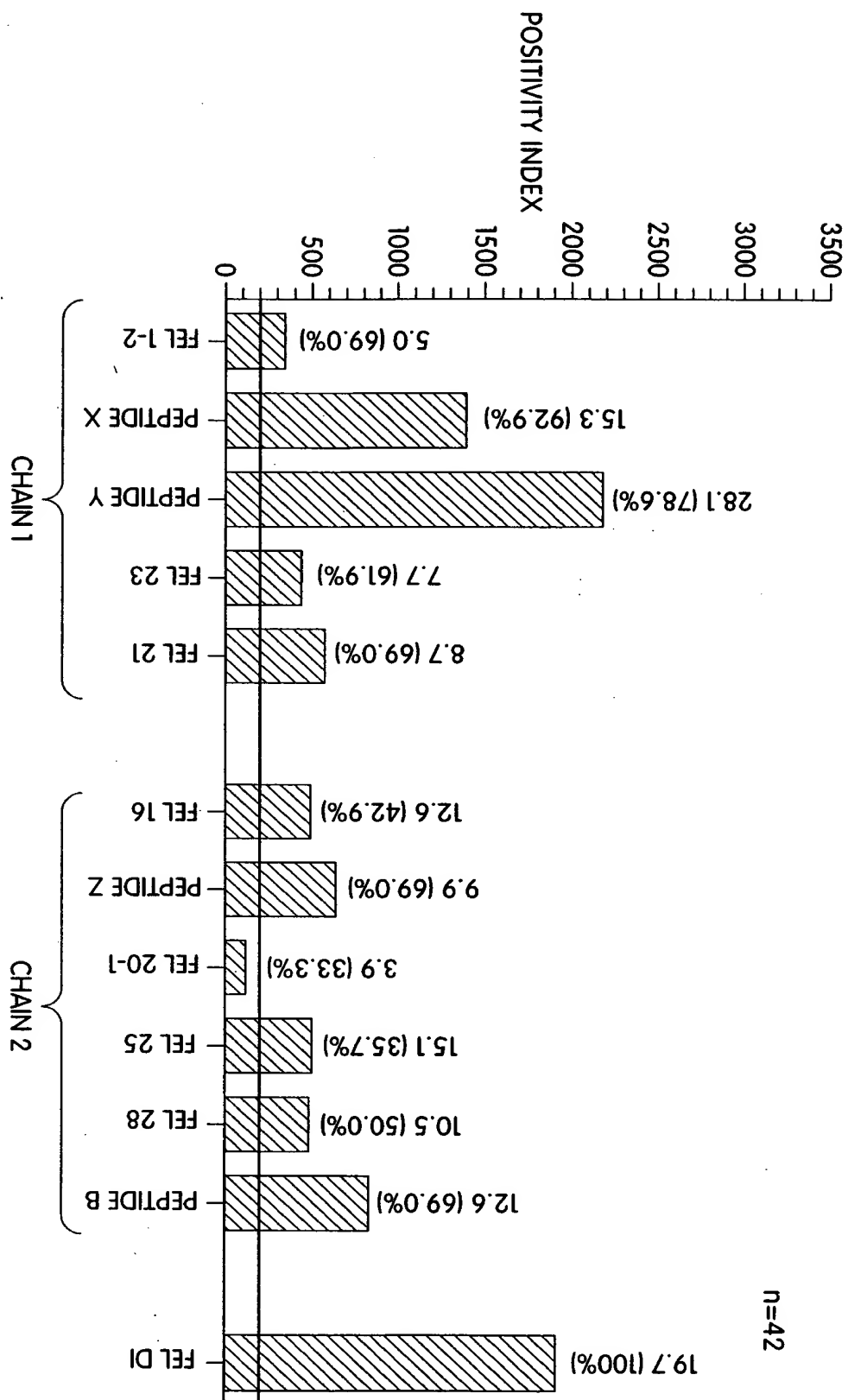


Fig. 22

Fig. 23





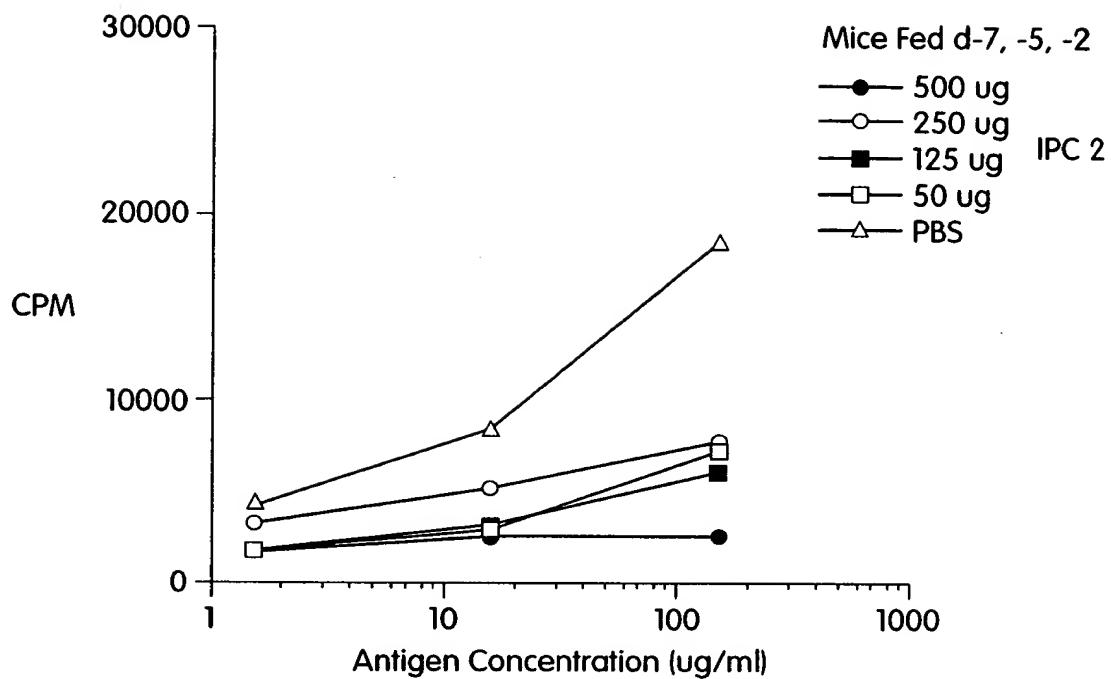


Fig. 24A

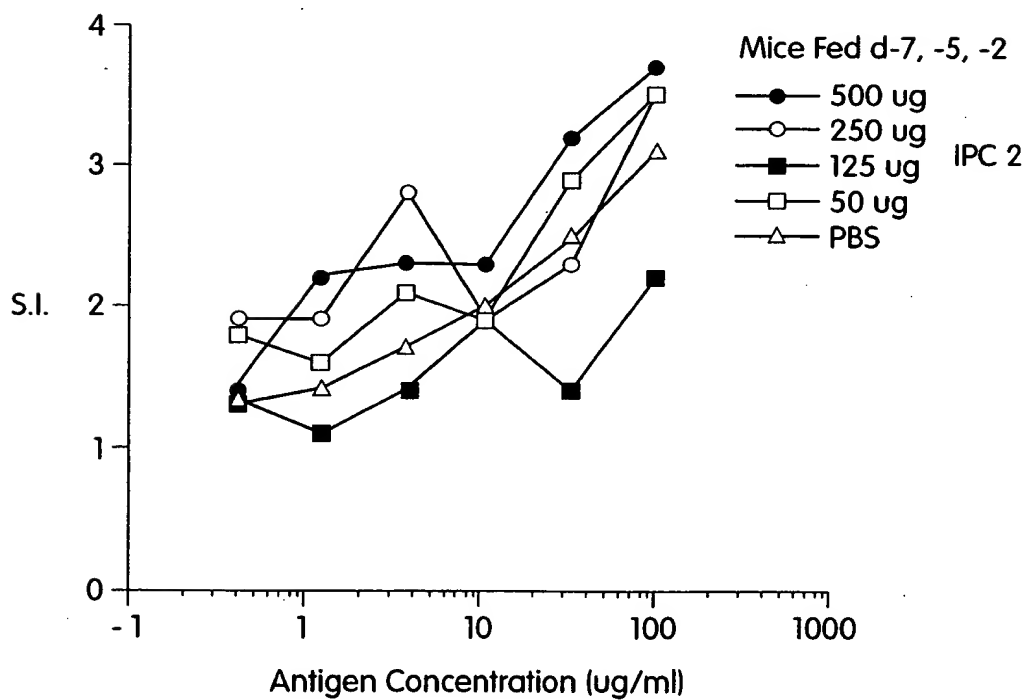


Fig. 24B

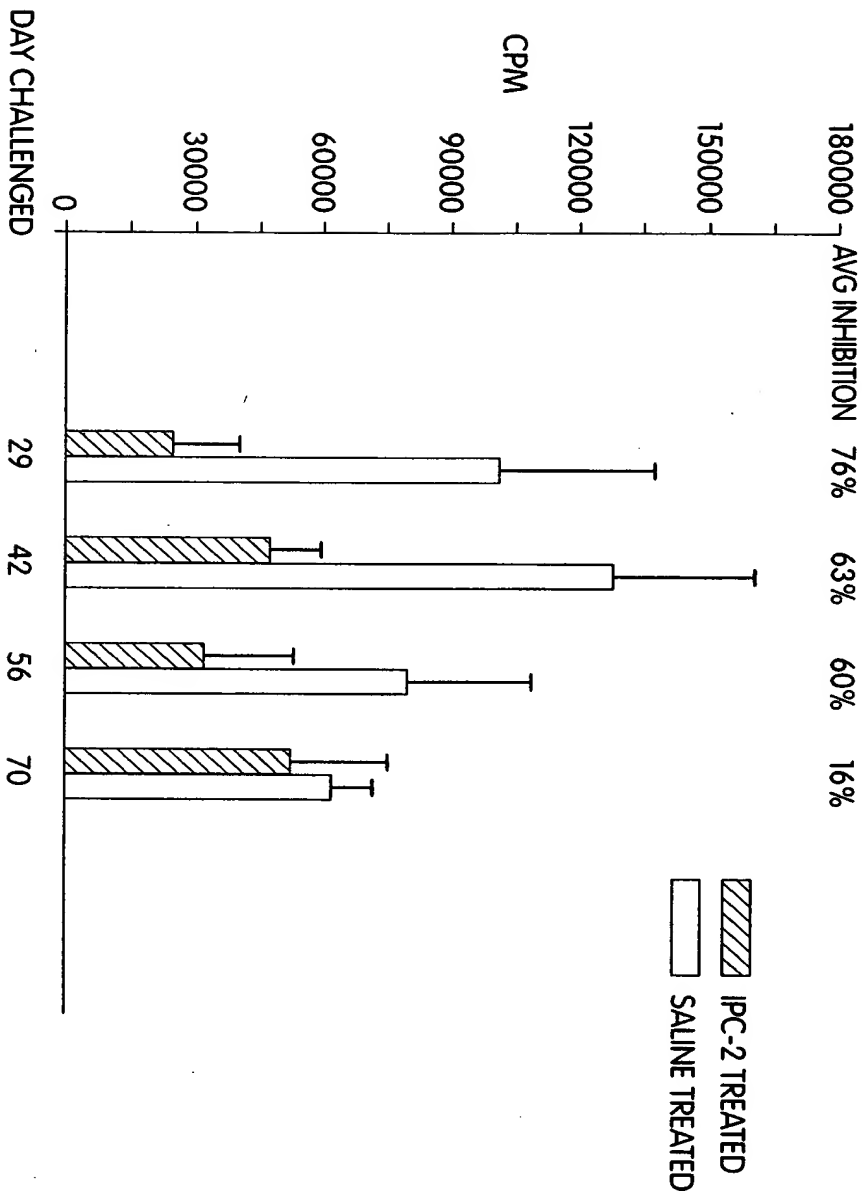


Fig. 25

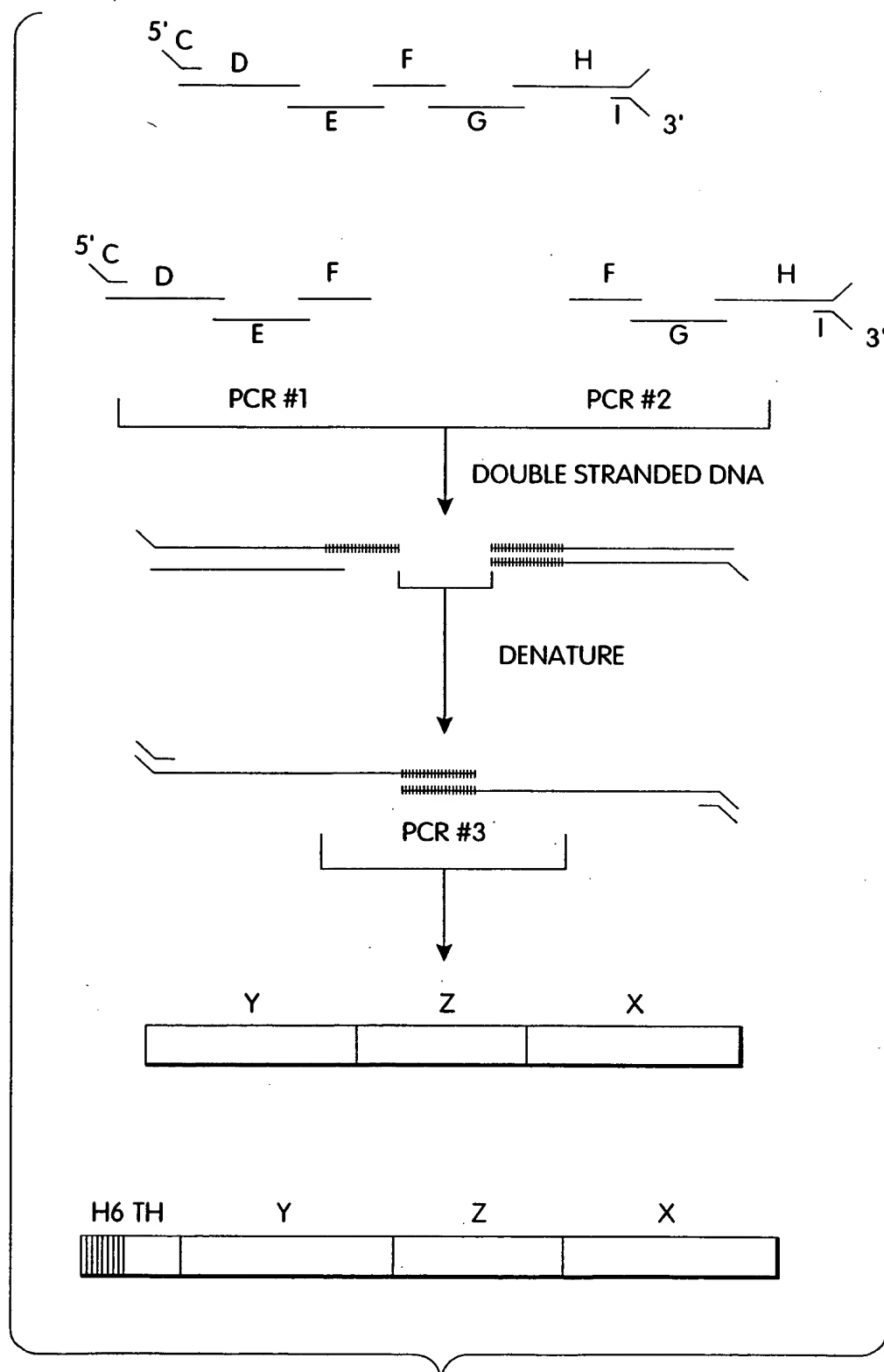


Fig. 26

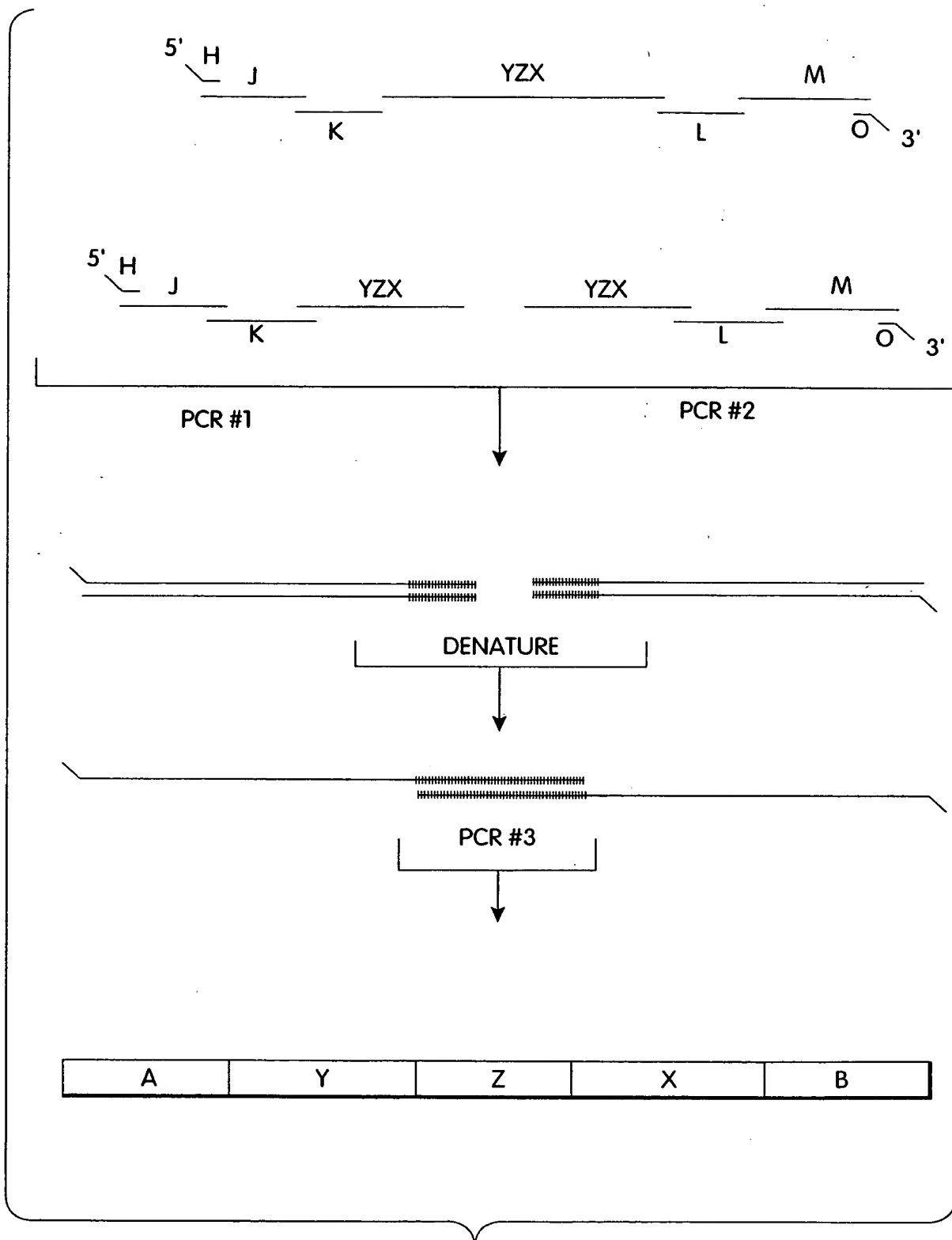


Fig. 27



C 5' BAM HI  
GGGGATCCAAAGCTCTGCCGGTGT 3'  
K A L P V V

D 5' BAM HI  
GGGGATCCAAAGCTCTGCCGGTGTCTGTGAAACGCTCGTATCCTGAAAAAACTGCGTTGACGCTAAATGACCGAA  
K A L P V V L E N A R I L K N C V D A K M T E  
GAAGACAAAGAA 3'  
E D K E

E 3' CTTCCTCTGTTCTTAAGAAGCGACAACGATTGCCATTGCTTGACGACGACCTGGACAGAGAC 5'  
E E D K E F F A V A N G N E L L L D L S L

F 5' CTGGACCTGTCTCTGACCACCAAGTTAACGCTACCGAACCGGAACGT 3'  
L D L S L T K V N A T E P E R

G 3' TGGCTTGGCCCTTGCACTTGCACTGGACAAGGACTGGCCCATGGGGCCTG 5'  
T E P E R K R D V D L F L T G T P D

H 5' ACCGGTACCCCGGACGAATACGTTGAACAGGTTGCTCAGTACAAAGCTCTGCCGGTTAGTCTAGACTGCAGAAG  
T G T P D E Y V E Q V A Q Y K A L P V - - XBAl PSTI  
CTTGGATCCCC 3'  
HINDIII ECORI

Fig. 28A



I 3' CGAGACGGCCAAATCATCAGATCTGACGTCCTTGAACCTAGGG 5'  
A L P V - - XBAI PSTI HINDIII ECORI

J 5' GGGGATCCGAAGAAGACAAAGAAAACGCTCTGTCTCTGCTG 3'  
BAM HI E E D K E N A L S L L

K 3' GACAGAGACGACCTGTTTATAGATGTGGAGAGCGGACTTTCGAGACGGCCAAACAGACCTT 5'  
L S L L D K I Y T S P L K A L P V L E

L 3' CGAGTCATGTTTCGAGACGGCCAAATACCCACTTCGACAAAGTCTTGTGGCAACTT 5'  
A Q Y K A L P V M G E A V Q N T V E

M 5' CAGAACACCGTTGAAGACCTGAAACTGAACACCCCTGGTCTGTAATGTAACCTGCAGAATTCCCC 3'  
Q N T V E D L K L N T L G R - PST I ECORI

N 5' GGGGATCCGAAGAAGACAAA 3'  
BAM HI E E D K

O 3' TGAACCCCTCTACTTACATTGACGTCCTTAAGGG 5'  
T L G R - PST I ECORI

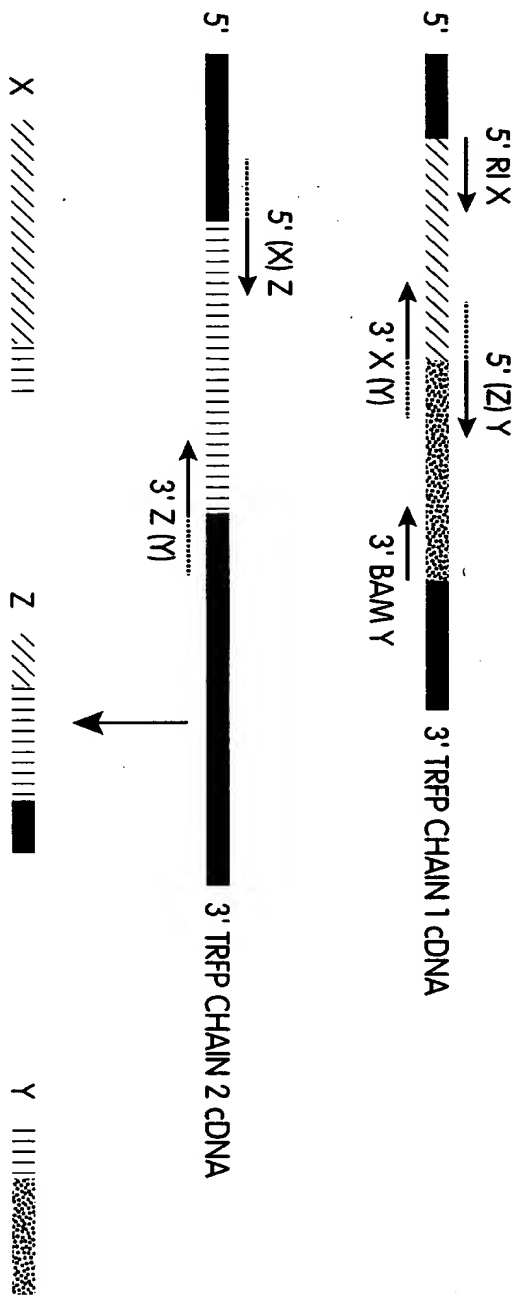
Fig. 28B



ATGGGTCACCAACCACCAACCAAGATTCTGGTTCGGCGTGATCC  
M G H H H H H H E F L V P R G S  
↓  
AAAGCTCTGCCGGTTGTTCTGGA<sup>1</sup>AAACGCTCGTATCCTGAAAAACTGC  
K A L P V V L E N A R I L K N C  
GTTGACGCTAAATGACCGAAGAAGACAAGAATTCTCGCTGTTGCT  
V D A K M T E E D K E F F A V A  
AACGTAACGAAC<sup>2</sup>TGCTGTGACCTGTCTCTGACCAAGTTAACCT  
N G N E L L L D L S L T K V N A  
ACCGAACCGGAACGTAACGTTGACCTGTTCCTGACCGGTACC  
T E P E R K R D V D L F L T G T  
CCGGACGAATACGTTGAACAAGTTGCTCAGTACAAGCTCTGCCGGTT  
P D E Y V E Q V A Q Y K A L P V

Fig. 29

# 1) PCR INDIVIDUAL EPITOPES



# 2) LINK ISOLATED EPITOPES BY POOLING/PCR

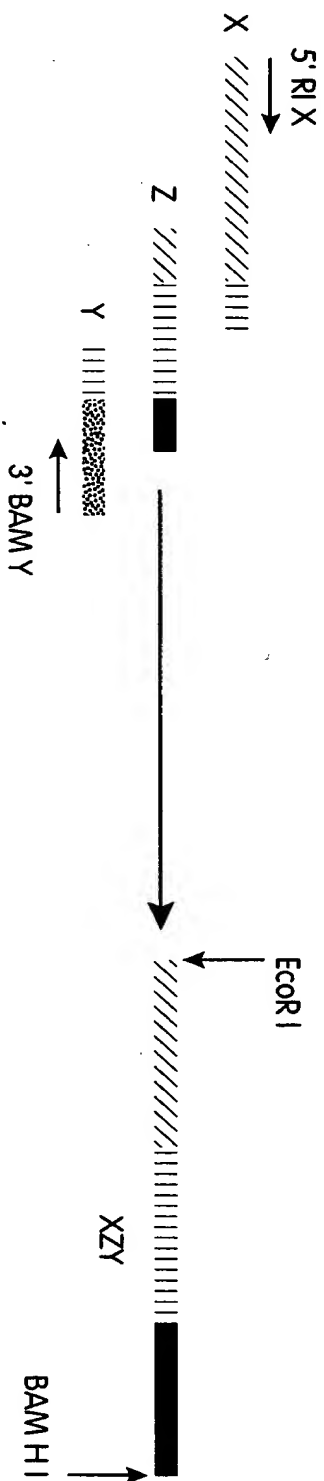


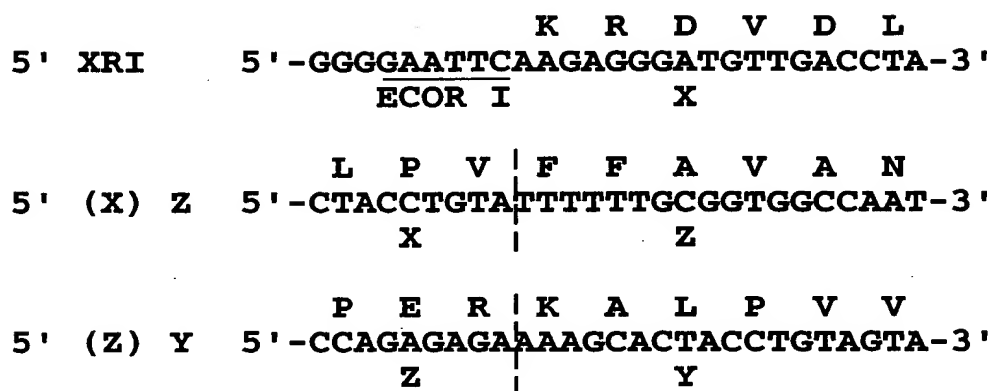
Fig. 30



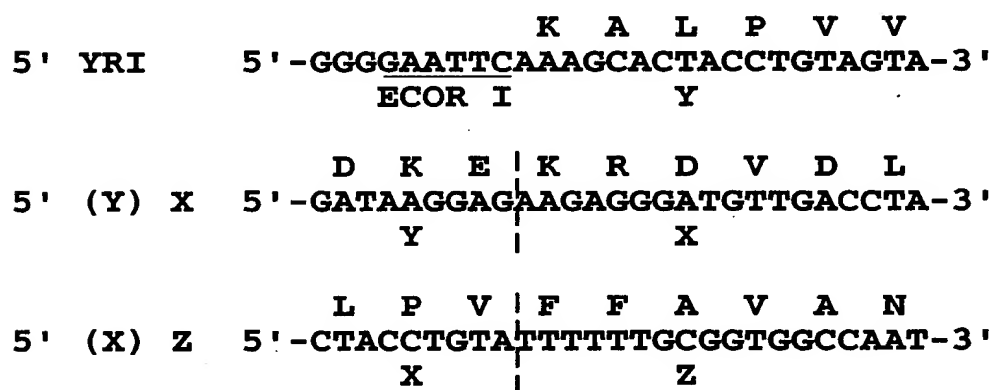


## 5' PRIMERS

### XZY CONSTRUCT



### YXZ CONSTRUCT



### ZXY CONSTRUCT

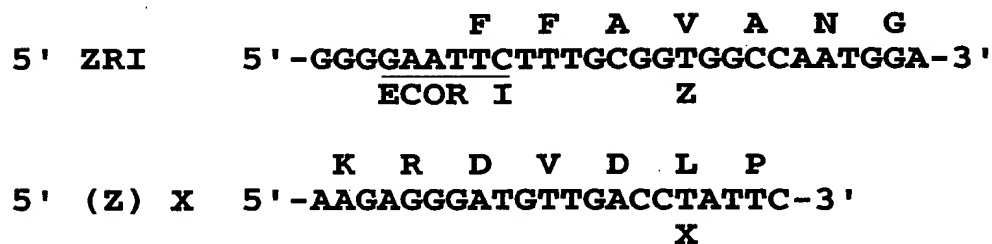


Fig. 31A



3' PRIMERS

XZY CONSTRUCT

3' X (Z) 5'- $\alpha$ N  $\alpha$ A  $\alpha$ V  $\alpha$ A  $\alpha$ F  $\alpha$ F |  $\alpha$ V  $\alpha$ P  $\alpha$ L  $\alpha$ A  $\alpha$ K  $\alpha$ Y  
Z X  
3' Z (Y) 5'- $\alpha$ L  $\alpha$ A  $\alpha$ K |  $\alpha$ R  $\alpha$ E  $\alpha$ P  $\alpha$ E  $\alpha$ T  $\alpha$ A  
Y Z  
3' Y BAM 5'- $\alpha$ STOP $\alpha$ E  $\alpha$ K  $\alpha$ D  $\alpha$ E  $\alpha$ E  $\alpha$ T  
BAMH I Y

YXZ CONSTRUCT

3' Y (X) 5'- $\alpha$ L  $\alpha$ D  $\alpha$ V  $\alpha$ D  $\alpha$ R  $\alpha$ K |  $\alpha$ E  $\alpha$ K  $\alpha$ D  $\alpha$ E  $\alpha$ E  $\alpha$ T  
X Y  
3' X (Z) 5'- $\alpha$ A  $\alpha$ F  $\alpha$ F |  $\alpha$ V  $\alpha$ P  $\alpha$ L  $\alpha$ A  $\alpha$ K  $\alpha$ Y  
Z X  
3' Z BAM 5'- $\alpha$ STOP $\alpha$ R  $\alpha$ E  $\alpha$ P  $\alpha$ E  $\alpha$ T  $\alpha$ A  
BAMH I Z

ZXY CONSTRUCT

3' Z (X) 5'- $\alpha$ L  $\alpha$ D  $\alpha$ V  $\alpha$ D  $\alpha$ R  $\alpha$ K |  $\alpha$ R  $\alpha$ E  $\alpha$ P  $\alpha$ E  $\alpha$ T  $\alpha$ A  $\alpha$ N  
X Z  
3' Y BAM 5'- $\alpha$ STOP $\alpha$ E  $\alpha$ K  $\alpha$ D  $\alpha$ E  $\alpha$ E  $\alpha$ T  $\alpha$ M  
BAMH I Y

Fig. 31B

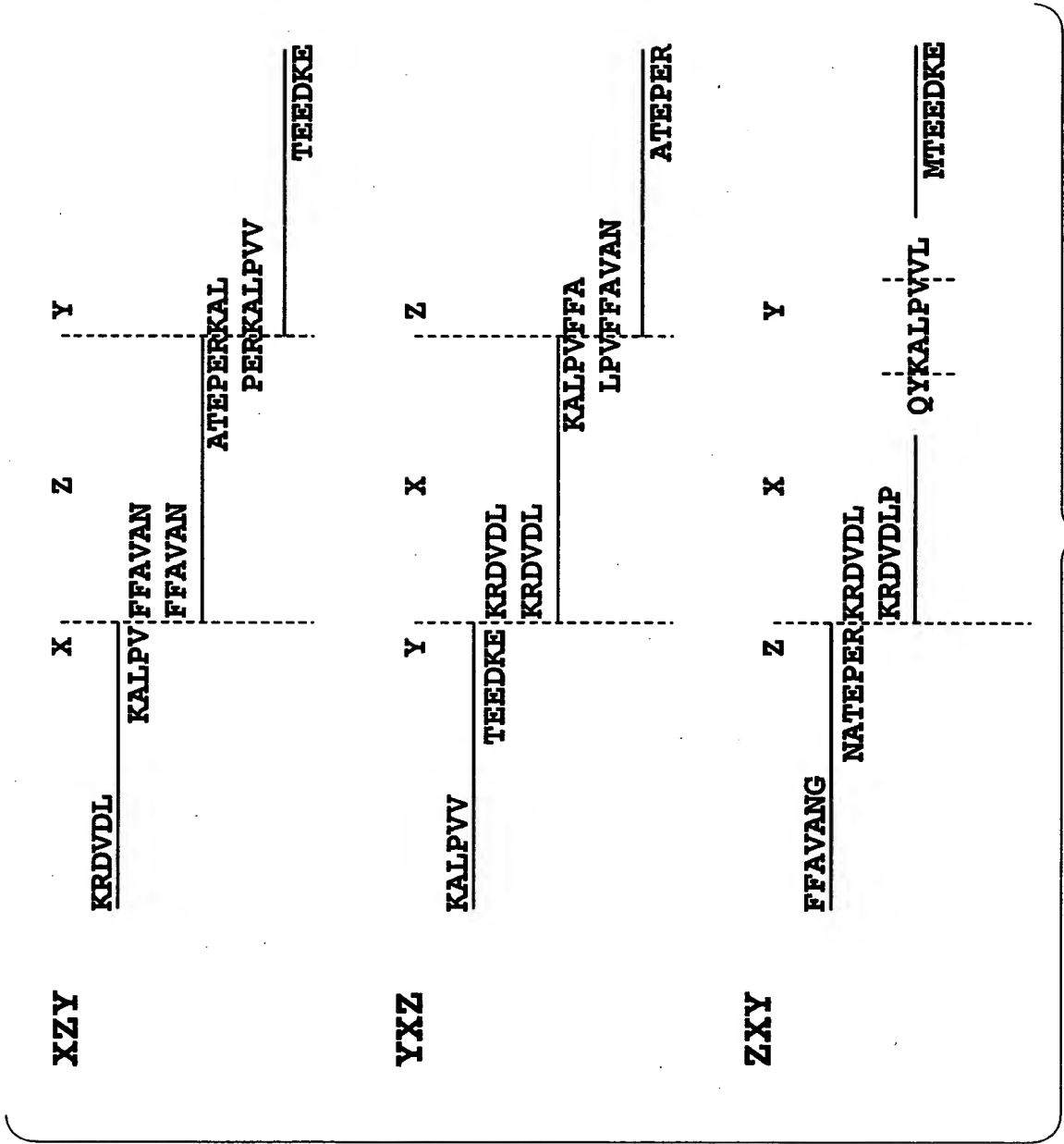


Fig. 32

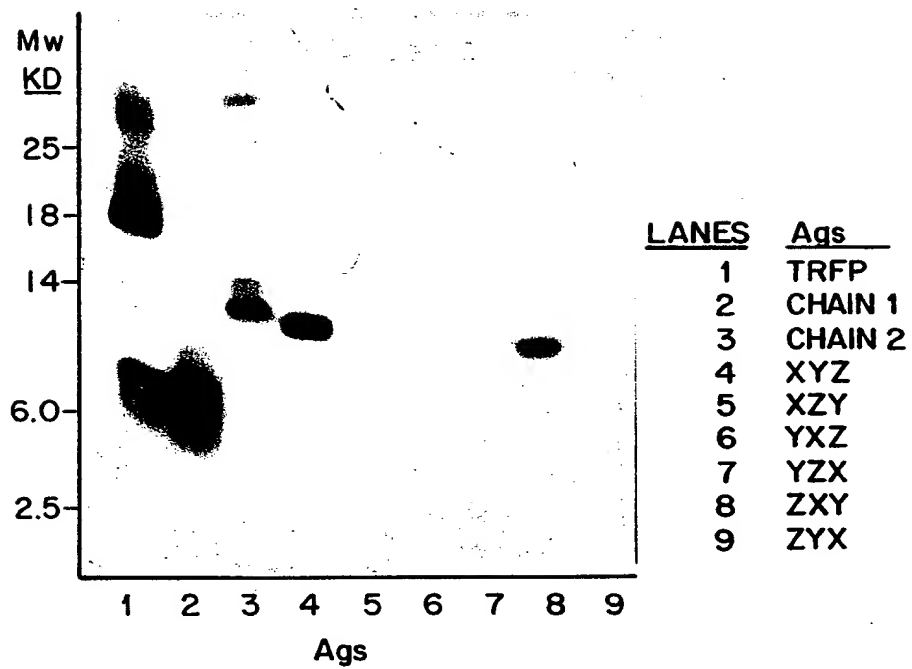


Fig. 33

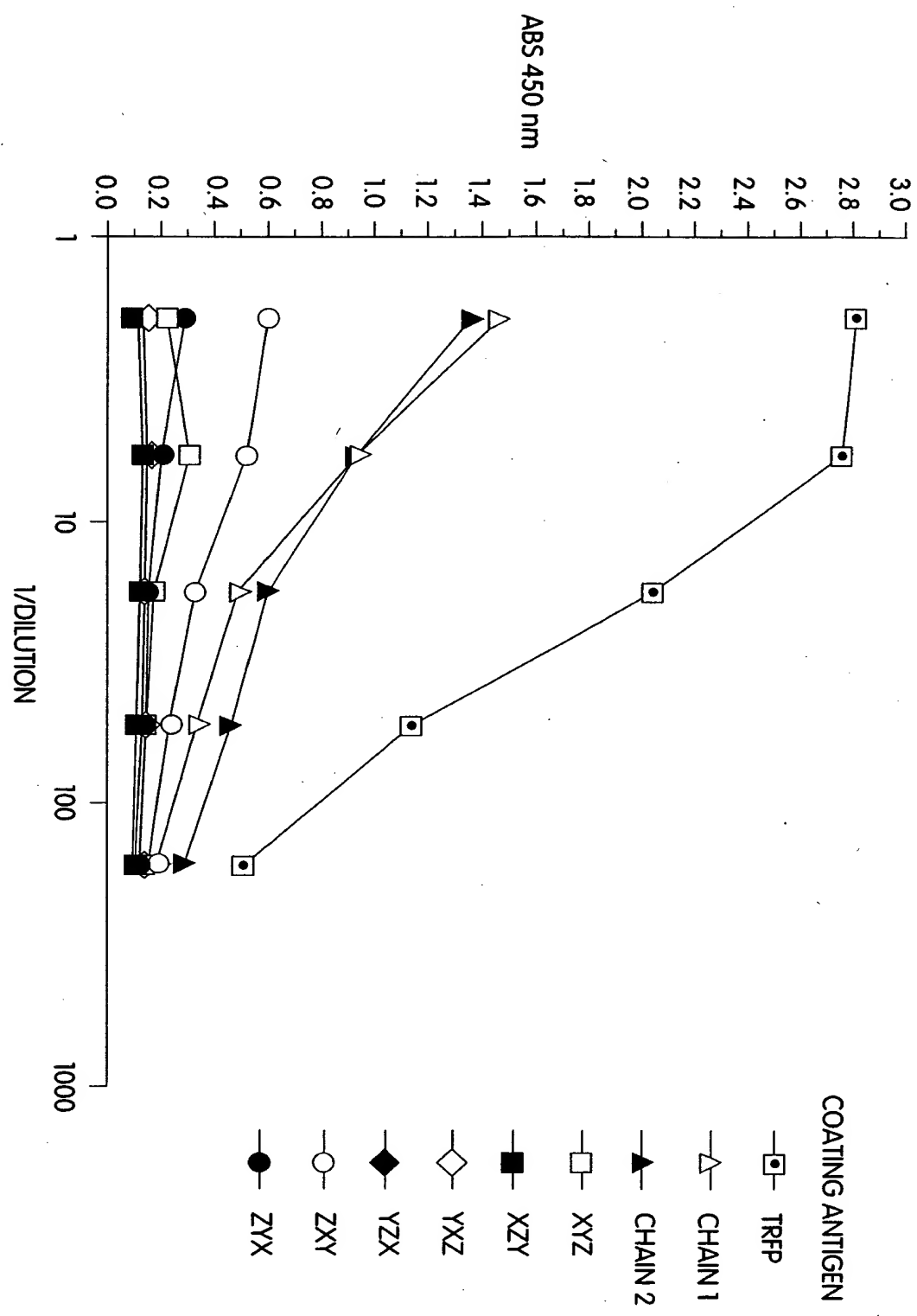


Fig. 34

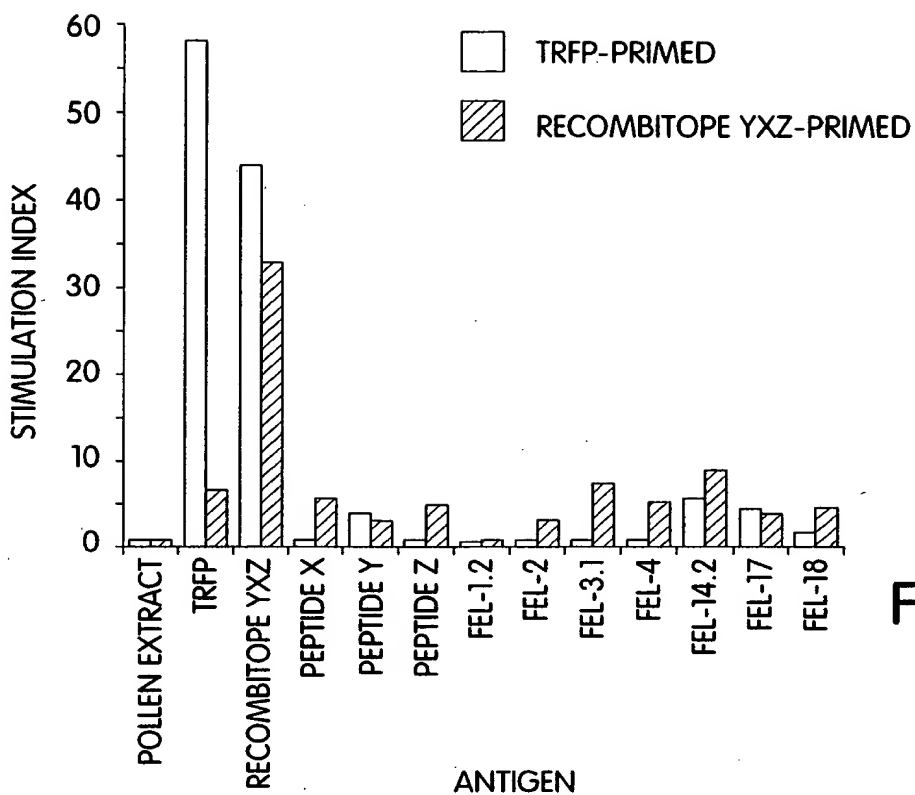


Fig. 35A

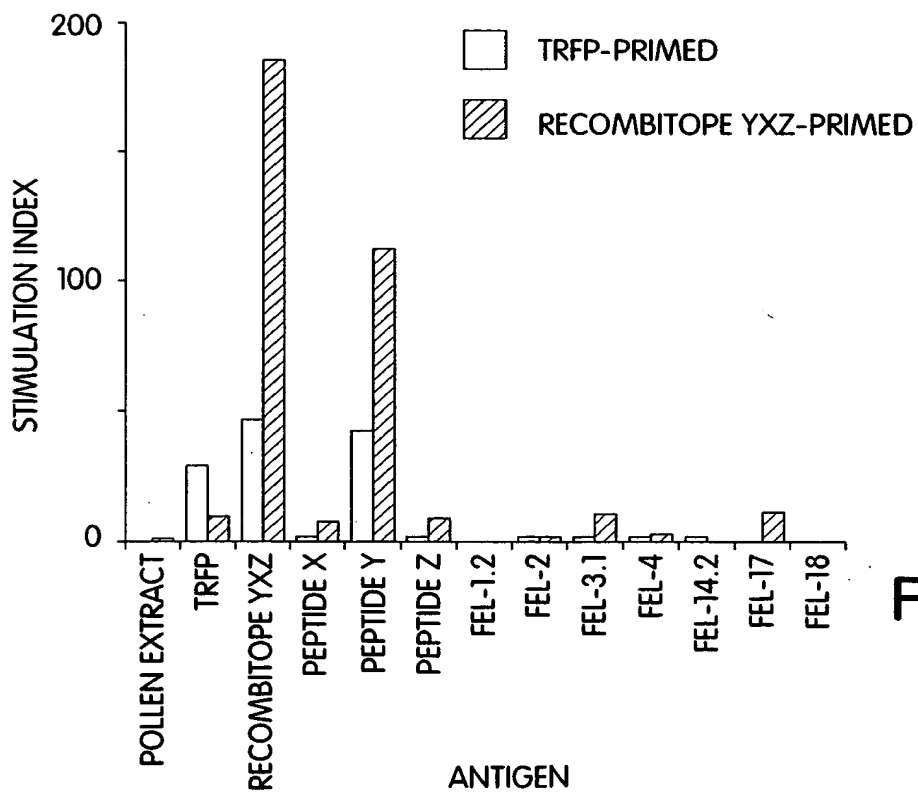


Fig. 35B

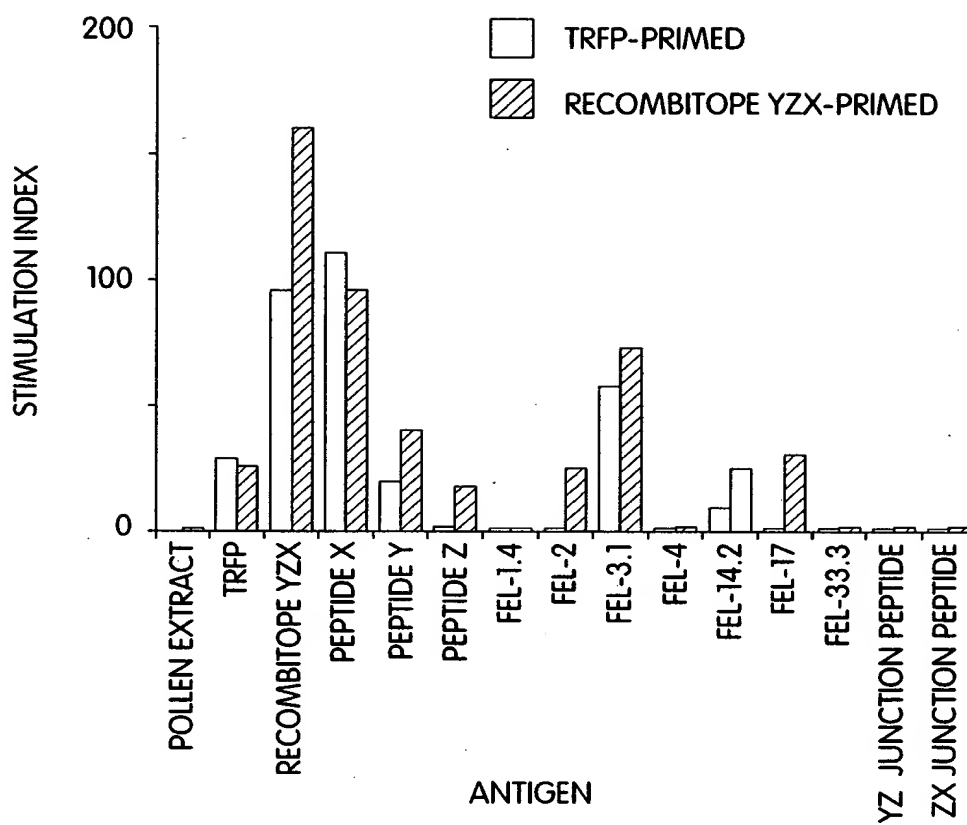


Fig. 35C

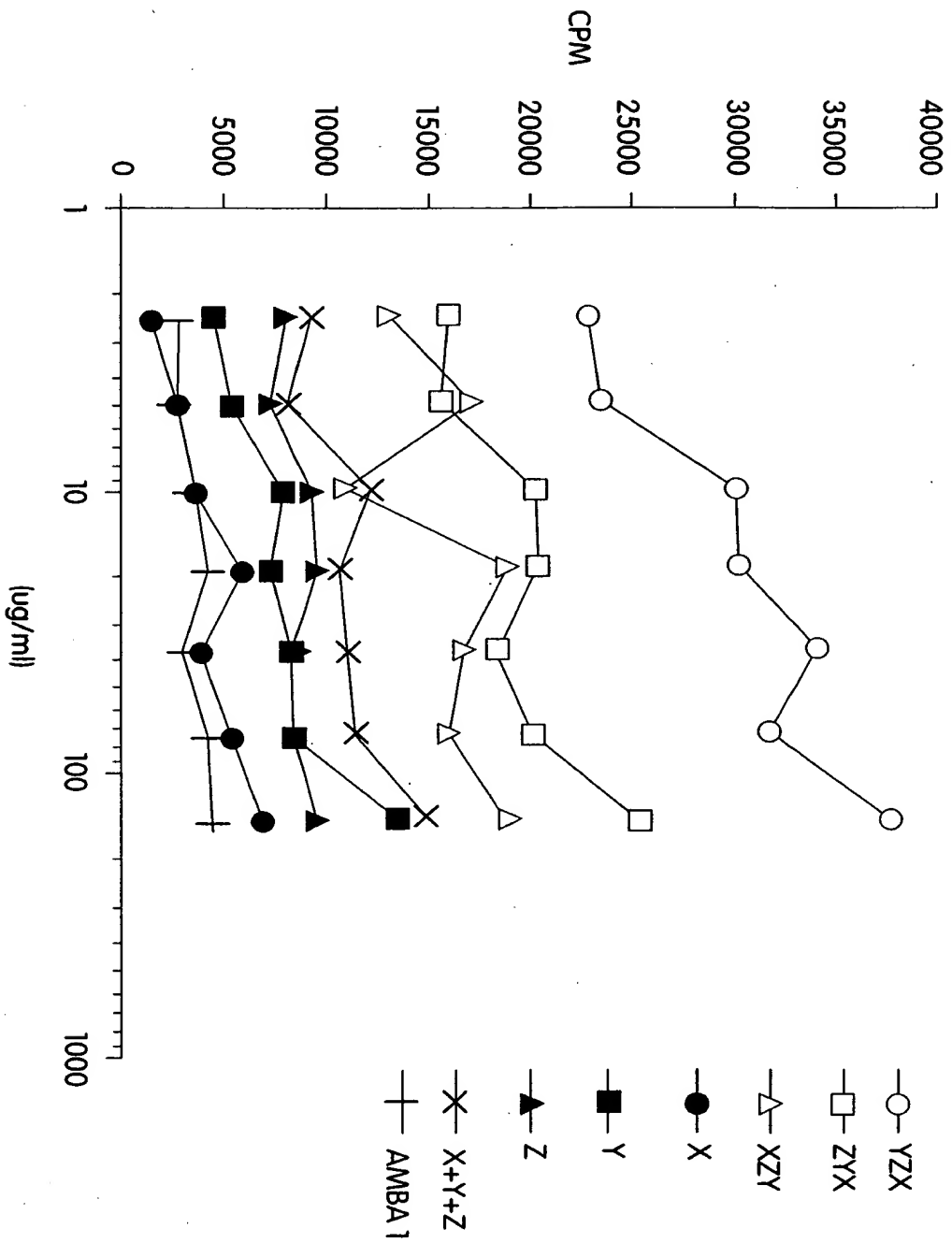


Fig. 36



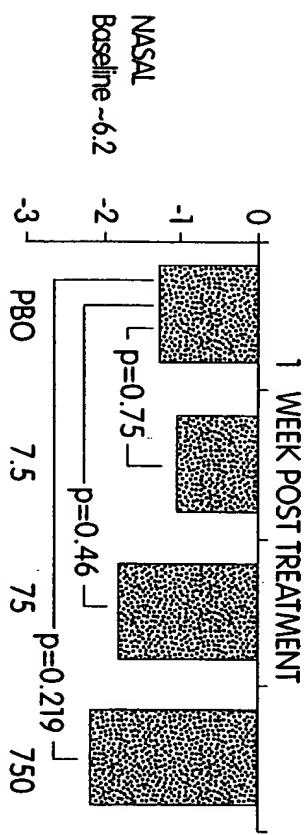


Fig. 37A

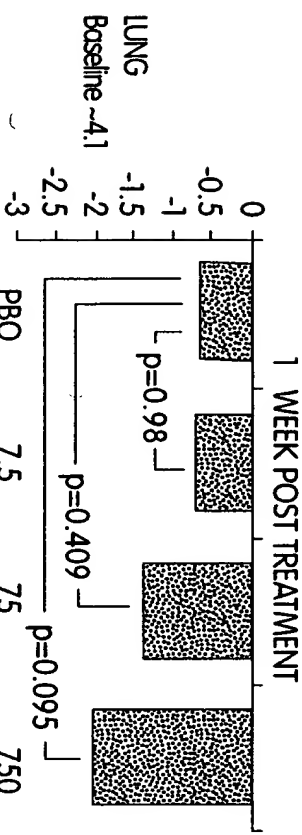


Fig. 37C

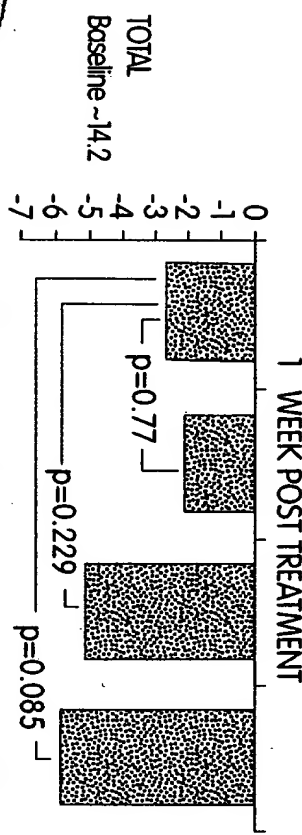


Fig. 37E

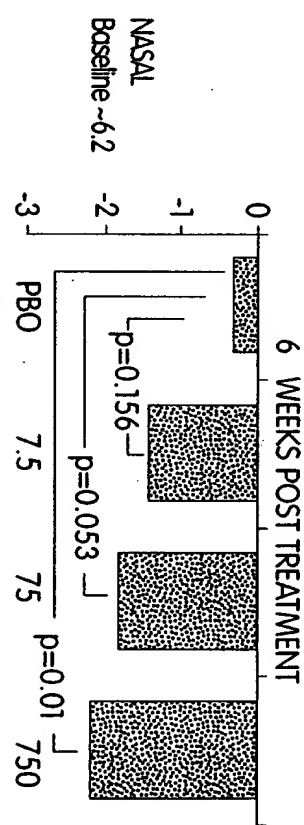


Fig. 37B

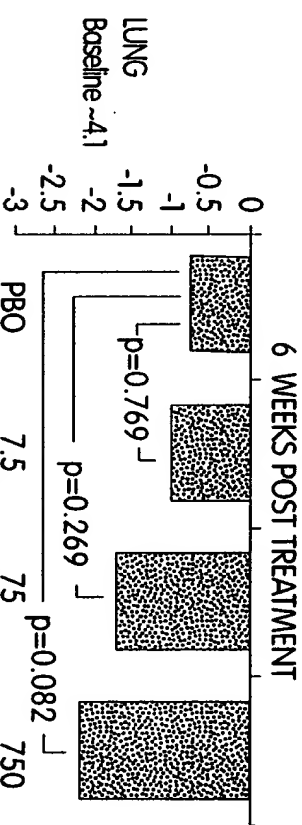


Fig. 37D

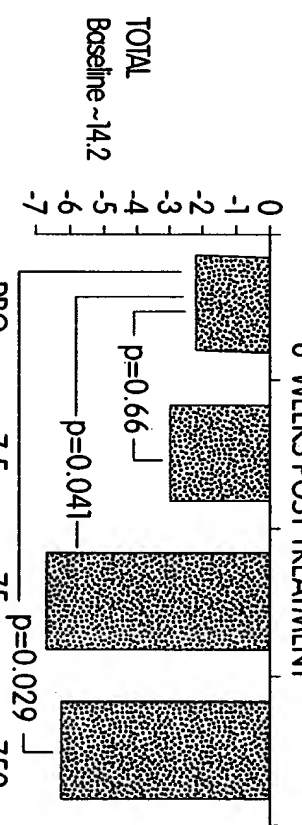


Fig. 37F